CLAIMS

1. A method for detecting the genotype in a nucleic acid sample, comprising the following step (a):

(a) analyzing two or more polymorphisms selected from the group consisting of the following (1) to (10) in a nucleic acid sample:

(1) polymorphism at the base number position 1019 of the connexin 37 gene;

(2) polymorphism at the base number position -863 of the tumor necrosis factor α gene;

(3) polymorphism at the base number position 242 of the NADH/NADPH oxidase p22 phox gene;

(4) polymorphism at the base number position -6 of the angiotensinogen gene:

(5) polymorphism at the base number position -219 of the apolipoprotein E gene;

(6) polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene;

(7) polymorphism at the base number position -482 of the apolipoprotein C-III gene;

(8) polymorphism at the base number position 1186 of the thrombospondin 4 gene;

(9) polymorphism at the base number position -819 of the interleukin-10 gene; and

(10) polymorphism at the base number position -592 of the interleukin-10 gene.

2. A method for detecting the genotype in a nucleic acid sample, comprising the following step (b):

(b) analyzing two or more polymorphisms selected from the group consisting of the following (11) to (15) in a nucleic acid sample:

(11) polymorphism at the base number position -1171 of the stromelysin 1 gene;

(12) polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(13) polymorphism at the base number position 1018 of the glycoprotein Ibα gene;

(14) polymorphism at the base number position 584 of the paraoxonase gene: and

(15) polymorphism at the base number position 4070 of the apolipoprotein E gene.

3. A method for detecting the genotype in a nucleic acid sample, comprising the following step (c):

(c) analyzing polymorphism at the base number position 4070 of the apolipoprotein E gene in a nucleic acid sample.

4. A method for diagnosing the risk of myocardial infarction, comprising the following steps (i) to (iii):

(i) analyzing two or more polymorphisms selected from the group consisting of the following (1) to (10) in a nucleic acid sample:

(1) polymorphism at the base number position 1019 of the connexin 37 gene;

(2) polymorphism at the base number position -863 of the tumor necrosis factor α gene;

(3) polymorphism at the base number position 242 of the NADH/NADPH oxidase p22 phox gene;

(4) polymorphism at the base number position -6 of the angiotensinogen gene:

(5) polymorphism at the base number position -219 of the apolipoprotein E gene;

(6) polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene;

(7) polymorphism at the base number position -482 of the apolipoprotein C-III gene;

(8) polymorphism at the base number position 1186 of the thrombospondin 4 gene;

(9) polymorphism at the base number position -819 of the interleukin-10 gene; and

(10) polymorphism at the base number position -592 of the interleukin-10 gene;

(ii) determining, based on the information about polymorphism which was obtained in the step (i), the genotype of the nucleic acid sample; and

(iii) assessing, based on the genotype determined, a genetic risk of myocardial infarction.

5. A method for diagnosing the risk of myocardial infarction, comprising the following steps (iv) to (vi):

(iv) analyzing two or more polymorphisms selected from the group consisting of the following (11) to (15) in a nucleic acid sample:

(11) polymorphism at the base number position -1171 of the stromelysin 1 gene;

(12) polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(13) polymorphism at the base number position 1018 of the

glycoprotein Ibα gene;

(14) polymorphism at the base number position 584 of the paraoxonase gene: and

(15) polymorphism at the base number position 4070 of the apolipoprotein E gene;

(v) determining, based on the information about polymorphism which was obtained in the step (i), the genotype of the nucleic acid sample; and

(vi) assessing, based on the genotype determined, a genetic risk of myocardial infarction.

6. A method for diagnosing the risk of myocardial infarction, comprising the following steps (vii) to (ix):

(vii) analyzing polymorphism at the base number position 4070 of the apolipoprotein E gene in a nucleic acid sample;

(viii) determining, based on the information about polymorphism which was obtained in the step (vii), the genotype of the nucleic acid sample; and

(ix) assessing, based on the genotype determined, a genetic risk of myocardial infarction.

7. A kit for detecting the genotype, comprising two or more of nucleic acids selected from the group consisting of the following (1) to (10):

(1) a nucleic acid for polymorphism analysis at the base number position 1019 of the connexin 37 gene;

(2) a nucleic acid for polymorphism analysis at the base number position -863 of the tumor necrosis factor α gene;

(3) a nucleic acid for polymorphism analysis at the base number position 242 of the NADH/NADPH oxidase p22 phox gene;

(4) a nucleic acid for polymorphism analysis at the base number position -6 of the angiotensinogen gene:

(5) a nucleic acid for polymorphism analysis at the base number position -219 of the apolipoprotein E gene;

(6) a nucleic acid for polymorphism analysis at the base number position 994 of the platelet-activating factor acetylhydrolase gene;

(7) a nucleic acid for polymorphism analysis at the base number position -482 of the apolipoprotein C-III gene;

(8) a nucleic acid for polymorphism analysis at the base number position 1186 of the thrombospondin 4 gene;

(9) a nucleic acid for polymorphism analysis at the base number position -819 of the interleukin-10 gene; and

(10) a nucleic acid for polymorphism analysis at the base number position -592 of the interleukin-10 gene.

8. A kit for detecting the genotype, comprising two or more of nucleic acids selected from the group consisting of the following (11) to (15):

(11) a nucleic acid for polymorphism analysis at the base number position -1171 of the stromelysin 1 gene;

(12) a nucleic acid for polymorphism analysis at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(13) a nucleic acid for polymorphism analysis at the base number position 1018 of the glycoprotein Ibα gene;

(14) a nucleic acid for polymorphism analysis at the base number position 584 of the paraoxonase gene: and

(15) a nucleic acid for polymorphism analysis at the base number position 4070 of the apolipoprotein E gene.

9. A kit for detecting the genotype, comprising a nucleic acid for polymorphism analysis at the base number position 4070 of the apolipoprotein E gene.

10. Fixed nucleic acids comprising the following two or more nucleic acid selected from the group consisting of the following (1) to (10) fixed to an insoluble support:

(1) a nucleic acid for polymorphism analysis at the base number position 1019 of the connexin 37 gene;

(2) a nucleic acid for polymorphism analysis at the base number position -863 of the tumor necrosis factor α gene;

(3) a nucleic acid for polymorphism analysis at the base number position 242 of the NADH/NADPH oxidase p22 phox gene;

(4) a nucleic acid for polymorphism analysis at the base number position -6 of the angiotensinogen gene:

(5) a nucleic acid for polymorphism analysis at the base number position -219 of the apolipoprotein E gene;

(6) a nucleic acid for polymorphism analysis at the base number position 994 of the platelet-activating factor acetylhydrolase gene;

(7) a nucleic acid for polymorphism analysis at the base number position -482 of the apolipoprotein C-III gene;

(8) a nucleic acid for polymorphism analysis at the base number position 1186 of the thrombospondin 4 gene;

(9) a nucleic acid for polymorphism analysis at the base number position -819 of the interleukin-10 gene; and

(10) a nucleic acid for polymorphism analysis at the base number position -592 of the interleukin-10 gene.

11. Fixed nucleic acids comprising the following two or more

nucleic acid selected from the group consisting of the following (11) to (15) fixed to an insoluble support:

(11) a nucleic acid for polymorphism analysis at the base number position -1171 of the stromelysin 1 gene;

(12) a nucleic acid for polymorphism analysis at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(13) a nucleic acid for polymorphism analysis at the base number position 1018 of the glycoprotein Ibα gene;

(14) a nucleic acid for polymorphism analysis at the base number position 584 of the paraoxonase gene: and

(15) a nucleic acid for polymorphism analysis at the base number position 4070 of the apolipoprotein E gene.

12. Fixed nucleic acids comprising a nucleic acid for polymorphism analysis at the base number position 4070 of the apolipoprotein E gene fixed to an insoluble support.